NOVEL HUMAN LEPTIN RECEPTOR GENE-RELATED PROTEIN Bailleul et al. PF-0111-3 CON

; '	101	330	13 TTG	3 GC	AGG	ig ctg		333	CCG	TGG	TAG	37 2 AA	3CS	3GA	46 AGC	AGC	130	5.5 330
	000	AGT	64 TCG	GGA	GAC	T3 ATG M	GCG A	GGC G	31 GTT 7	AAA K	GCT A	91 910 1	GTG ;	GCA A	100 TTA 1	TCC s	TTC	109 AGT S
	333 3	GCT A	118 ATT I	GGA G	CTG L	127 ACT T	TTT E	CTT	136 ATG M	CTG L	gga g	145 TGT C	SCC A	TTA L	154 EAG E	gar D	TAT Y	163 330 3
	STT 7	TAC Y	172 TGG W	SCC CCC	TTA L	181 TTC F	GTC V	CTG 1	190 ATT I	TTC E	CAC H	199 3GC G	AIC I	TCC S	209 CCC P	ATC I	333 2	
	TTC E	ATT I	026 3CC A	AAA K	AGA R	235 GTC V	ACC T	TAT Y	244 GAC D	TCA S	GAT D	253 GCA A	ACC T	AGT S	262 AGT S	GCC A	TGT C	371 353 R
	3 A A E	CTG L	230 GCA A	TAT	TTC E	TTC	ACT T	ACT	GGA	ATT	GIT V	FIT	TCT S	GCC	TTT	GGA G	 	325 CCT P
	GTT 7	ATT I	334 CTT L	GCT	CGT R	GTG	GCT	GTG V	ATC	AAA	TGG	GGA	GCC	TGC	GGC	CTT L	JIG	379 ITG L
	GCA A	GGC G	388 AAT N	GCA A	GIC V	397 ATT I	TTC F	CTT L	406 ACA T	ATT I	CAA Q	415 GGG G	TTT F	TTC F	424 CTT L	ATA I	TTT	433 GGA G
	AGA R	GGA G	GAT	GAT	TTT F	AGC	TGG	GAG	CAG	TGG	TAG	469 CAC	TTT	ATT	478 CTG	ATT	ACA	497 313
	CAT	IGA	496 ATT	TCT	TAG	505 AAC	TCA	TAC	514 TAT	CTG	TAT	523 ACA	īGī	SCA	532 CAT	3CG	3CA	541 TTT
	TAC	TAT	550 GAA	ATT	TAA	559 TAT	GCT	GGG	56 8 TTT	TTT	AAT	577 ACC	TTT	ATA	586 TAT	CAT	GIT	595 CAC
	TTT	AAG	604 AAA	GAC	TTC	613 ATA	agt	AGG	622 AGA	TGA	GIT	631 TTA	TTC	TCA	640 GCA	AAT	AGA	649 CCT
	FTC	AAA	65 8 T TT	AG A	TTA	667 TGT	TAC	TCA	676 AAT	TAT	GIT	685 ACT	īGī	TTG	694 <i>G</i> CT	GTT	CAT	703 TTA

FIGURE 1A

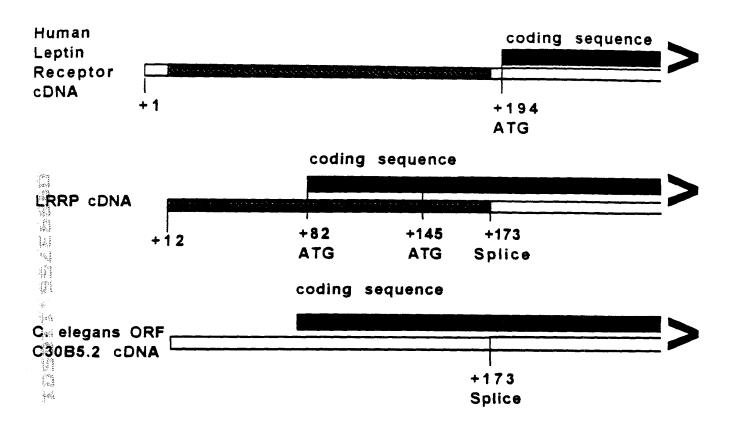
FTC	ACG									75 7 3 37
TAT	ЗСА	766 GTG								
sc r	3AA		CTC							
īGĪ	AGT									

FIGURE 1B

The Electronic Northern for Clone: 492703 and Stringency >= 50

Liprary	Lib Description	Abun	Pot Abun
RATRNOTSI	heart, right atrium, 51 F		0.0861
SYNCRABCI	synovium, hip, rheumatoid, 68 F	4	0.0779
LIVRNOMSI	liver, 49 M, WM	:	0.0254
PLACNOB01	placenta, neonatal F	:	0.0225
BRSTNOTCL	breast, 56 F	:	0.0192
HNT2AGT01	nNT-2 cell line, post-mitotic neurons	:	0.0190
HNT2NCT01	nNT-2 cell line, teratocarcinoma, control	:	0.0172
BRSTTUT03	preast tumor, 58 F, match to BRSTNOTOS	1	0.0148
COLNFETO2	colon, fetal F	:	0.0142
UCMCL5T01	lymphocytes (umbilical cord), treated IL-5	•	0.0125
MELANOMOL	me_anocytes, M, NORM, WM	•	0.0108
PLACNOM02	placenta, neonatal F, NORM, WM	:	0.0056

FIGURE 2



* Numbering relative to human leptin receptor

Hatched area represents identical sequences

FIGURE 3

```
M - - - - - - - - - - - - - - A G V KAL V A L S F S G A SEQ ID NO-1

M C C H I H I Q C F D C C S M K N T I LAV A L A F A G V SEQ ID NO-3

M - - - - - M E F K V S P L T K I I - - - - - S L S G F SEQ ID NO-4

16

I G L T F L M - - L G C A L E D Y G V Y W P L F V L I F H G SEQ ID NO-1

31

Y G L T F L V - - L G C A L P R Y G T W T P MM F V I T F Y V SEQ ID NO-3

19

L A L G F L L V I L S C A L - - F H N Y Y P L F D I L I F L SEQ ID NO-4

44

L S P I P H F I A K R V T - Y D S D - - - A T S S - A C R E SEQ ID NO-4

45

L S P Y P L L I A R R - - - F Q E D - - - M T G T N A C I E SEQ ID NO-3

47

L A P I P N T I F N A G N K Y H T S D F M S D S S N T G Q D SEQ ID NO-4

69

L A Y F F T T G I V V S A F G F P V I L A R V A V I K W G A SEQ ID NO-3

77

L A H F L T G I V I S A F A L P I V L A H A G T I A M S A SEQ ID NO-3

78

99

C G L V L A G N A V I F L T I Q G F F L I F G R G D D F S W SEQ ID NO-3

107

113

107

C I M C M I G G L I I Y S S I V I F K W F F K K D F N E D D SEQ ID NO-4

SEQ ID NO-3

129

SEQ ID NO-3

SEQ ID NO-3
```

FIGURE 4



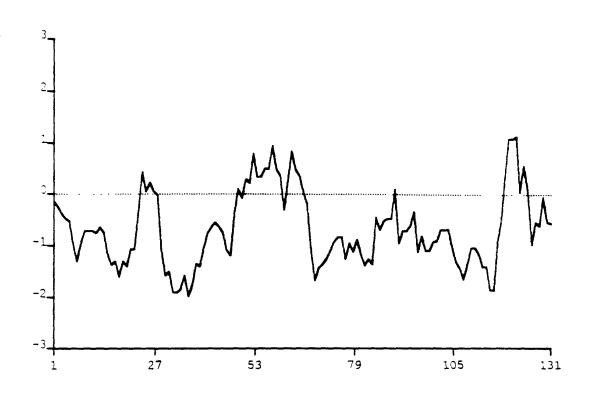


FIGURE 5

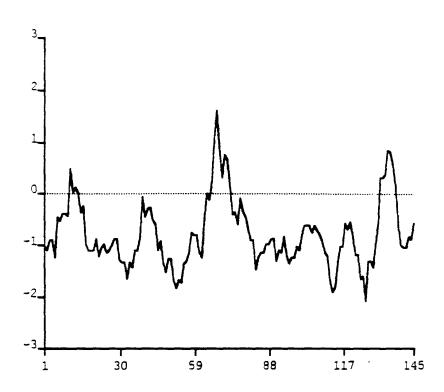
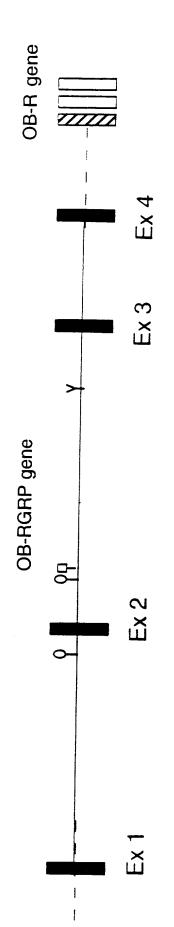


FIGURE 6

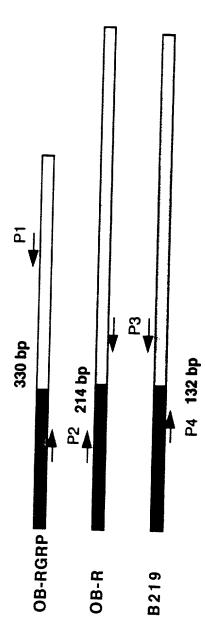
Human genomic organization of OB-RGRP



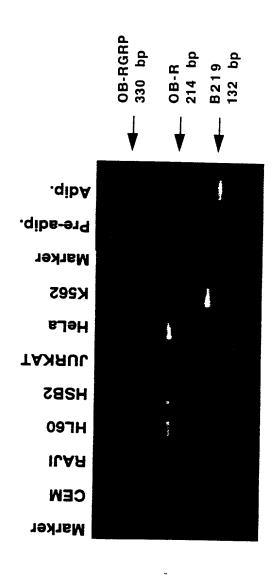
Exon/intron junctions of OB-RGRP gene

laLeuValAlaLeuSer ctttggctttalttttcacagCTCTCGTGGATFFATGG	yValTyrTrpProLeu (t)10ggatttgcctgggtccaactgacagCGFTTRCTGCCCCTTA	IleLysTrpGlyAla tectettettettetteagATCAAATGGGGAGGG
INTRON 1	INTRON 2 4.5 KB	INTRON 3 2.0 KB
MetAlaGlyValLysA ATGGCGGGCGTTAAAGgtacatcgcg	AlaLeuGluAspTyrGl GCCTTAGAGGATTATGGgtaagtt	LeuAlaArgValAlaVal CTTGCTCGTGTGGCTGTGgtaagttt

FIGURE 7



FIGURE



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